RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: ___10/788,489___

Source: ___IFWO___

Date Processed by STIC: ___04/12/2006___

ENTERED

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        RAW SEQUENCE LISTING            DATE: 04/12/2006
        PATENT APPLICATION:  US/10/788,489    TIME: 12:28:49

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        Output Set: N:\CRF4\04122006\J788489.raw

 1 <110> APPLICANT: CARILLO, Serge
 2        BLANCHARD, Jean-Marie
 3        PIECHACZYK, Marc
 4 <120> TITLE OF INVENTION: METHOD OF CANCER TREATMENT BY P53 PROTEIN CONTROL
 5 <130> FILE REFERENCE: ST94037A-US
 6 <140> CURRENT APPLICATION NUMBER: US/10/788,489
 7 <141> CURRENT FILING DATE: 2004-03-01
 8 <150> PRIOR APPLICATION NUMBER: US/09/405,920
 9 <151> PRIOR FILING DATE: 1999-09-24
10 <150> PRIOR APPLICATION NUMBER: 08/737,953
11 <151> PRIOR FILING DATE: 1996-11-27
12 <150> PRIOR APPLICATION NUMBER: FR94/06583
13 <151> PRIOR FILING DATE: 1994-05-31
14 <150> PRIOR APPLICATION NUMBER: WO PCT/FR95/00670
15 <151> PRIOR FILING DATE: 1995-05-22
16 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2085
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(2085)
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29       1               5                  10                  15
30      gta aaa aca gaa cct gag aag aag tca cag tca acc aag ctg tct gtg    96
31      Val Lys Thr Glu Pro Glu Lys Lys Ser Gln Ser Thr Lys Leu Ser Val
32                       20                  25                  30
33      gtt cat gag aaa aaa tcc caa gaa gga aag cca aaa gaa cac aca gag   144
34      Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu
35               35                  40                  45
36      cca aaa agc cta ccc aag cag gca tca gat aca gga agt aac gat gct   192
37      Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala
38           50                  55                  60
39      cac aat aaa aaa gca gtt tcc aga tca gct gaa cag cag cca tca gag   240
40      His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu
41       65                  70                  75                  80
42      aaa tca aca gaa cca aag act aaa cca caa gac atg att tct gct ggt   288
43      Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly
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45      gga gag agt gtt gct ggt atc act gca ata tct ggc aag ccg ggt gac   336
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47                  100                 105                 110
48      aag aaa aaa gaa aag aaa tca tta acc cca gct gtg cca gtt gaa tct   384
49      Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser
50                  115                 120                 125
51      aaa ccg gat aaa cca tcg gga aag tca ggc atg gat gct gct ttg gat   432
52      Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp
53                  130                 135                 140
54      gac tta ata gat act tta gga gga cct gaa gaa act gaa gaa gaa aat   480
55      Asp Leu Ile Asp Thr Leu Gly Gly Pro Glu Glu Thr Glu Glu Glu Asn
56      145                 150                 155                 160
57      aca acg tat act gga cca gaa gtt tca gat cca atg agt tcc acc tac   528
58      Thr Thr Tyr Thr Gly Pro Glu Val Ser Asp Pro Met Ser Ser Thr Tyr
59                  165                 170                 175
60      ata gag gaa ttg ggt aaa aga gaa gtc aca att cct cca aaa tat agg   576
61      Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg
62                  180                 185                 190
63      gaa cta ttg gct aaa aag gaa ggg atc aca ggg cct cct gca gac tct   624
64      Glu Leu Leu Ala Lys Lys Glu Gly Ile Thr Gly Pro Pro Ala Asp Ser
65                  195                 200                 205
66      tca aaa ccc ata ggg cca gat gat gct ata gac gcc ttg tca tct gac   672
67      Ser Lys Pro Ile Gly Pro Asp Asp Ala Ile Asp Ala Leu Ser Ser Asp
68                  210                 215                 220
69      ttc acc tgt ggg tcg cct aca gct gct gga aag aaa act gaa aaa gag   720
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71      225                 230                 235                 240
72      gaa tct aca gaa gtt tta aaa gct cag tca gca ggg aca gtc aga agt   768
73      Glu Ser Thr Glu Val Leu Lys Ala Gln Ser Ala Gly Thr Val Arg Ser
74                  245                 250                 255
75      gct gct cca ccc caa gag aag aaa aga aag gtg gag aag gat aca atg   816
76      Ala Ala Pro Pro Gln Glu Lys Lys Arg Lys Val Glu Lys Asp Thr Met
77                  260                 265                 270
78      agt gat caa gca ctc gag gct ctg tcg gct tca ctg ggc acc cgg caa   864
79      Ser Asp Gln Ala Leu Glu Ala Leu Ser Ala Ser Leu Gly Thr Arg Gln
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81      gca gaa cct gag ctc gac ctc cgc tca att aag gaa gtc gat gag gca   912
82      Ala Glu Pro Glu Leu Asp Leu Arg Ser Ile Lys Glu Val Asp Glu Ala
83                  290                 295                 300
84      aaa gct aaa gaa gaa aaa cta gag aag tgt ggt gag gat gat gaa aca   960
85      Lys Ala Lys Glu Glu Lys Leu Glu Lys Cys Gly Glu Asp Asp Glu Thr
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87      atc cca tct gag tac aga tta aaa cca gcc acg gat aaa gat gga aaa   1008
88      Ile Pro Ser Glu Tyr Arg Leu Lys Pro Ala Thr Asp Lys Asp Gly Lys
89                  325                 330                 335
90      cca cta ttg cca gag cct gaa gaa aaa ccc aag cct cgg agt gaa tca   1056
91      Pro Leu Leu Pro Glu Pro Glu Glu Lys Pro Lys Pro Arg Ser Glu Ser
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93      gaa ctc att gat gaa ctt tca gaa gat ttt gac cgg tct gaa tgt aaa   1104
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Input Set : **N:\Crf3\RULE60\10788489.raw**
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 96      gag aaa cca tct aag cca act gaa aag aca gaa gaa tct aag gcc gct    1152
 97      Glu Lys Pro Ser Lys Pro Thr Glu Lys Thr Glu Glu Ser Lys Ala Ala
 98          370             375             380
 99      gct cca gct cct gtg tcg gag gct gtg tct cgg acc tcc atg tgt agt    1200
100      Ala Pro Ala Pro Val Ser Glu Ala Val Ser Arg Thr Ser Met Cys Ser
101      385             390             395             400
102      ata cag tca gca ccc cct gag ccg gct acc ttg aag ggc aca gtg cca    1248
103      Ile Gln Ser Ala Pro Pro Glu Pro Ala Thr Leu Lys Gly Thr Val Pro
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105      gat gat gct gta gaa gcc ttg gct gat agc ctg ggg aaa aag gaa gca    1296
106      Asp Asp Ala Val Glu Ala Leu Ala Asp Ser Leu Gly Lys Lys Glu Ala
107              420             425             430
108      gat cca gaa gat gga aaa cct gtg atg gat aaa gtc aag gag aag gcc    1344
109      Asp Pro Glu Asp Gly Lys Pro Val Met Asp Lys Val Lys Glu Lys Ala
110              435             440             445
111      aaa gaa gaa gac cgt gaa aag ctt ggt gaa aaa gaa gaa aca att cct    1392
112      Lys Glu Glu Asp Arg Glu Lys Leu Gly Glu Lys Glu Glu Thr Ile Pro
113          450             455             460
114      cct gat tat aga tta gaa gag gtc aag gat aaa gat gga aag cca ctc    1440
115      Pro Asp Tyr Arg Leu Glu Glu Val Lys Asp Lys Asp Gly Lys Pro Leu
116      465             470             475             480
117      ctg cca aaa gag tct aag gaa cag ctt cca ccc atg agt gaa gac ttc    1488
118      Leu Pro Lys Glu Ser Lys Glu Gln Leu Pro Pro Met Ser Glu Asp Phe
119              485             490             495
120      ctt ctg gat gct ttg tct gag gac ttc tct ggt cca caa aat gct tca    1536
121      Leu Leu Asp Ala Leu Ser Glu Asp Phe Ser Gly Pro Gln Asn Ala Ser
122              500             505             510
123      tct ctt aaa ttt gaa gat gct aaa ctt gct gct gcc atc tct gaa gtg    1584
124      Ser Leu Lys Phe Glu Asp Ala Lys Leu Ala Ala Ala Ile Ser Glu Val
125          515             520             525
126      gtt tcc caa acc cca gct tca acg acc caa gct gga gcc cca ccc cgt    1632
127      Val Ser Gln Thr Pro Ala Ser Thr Thr Gln Ala Gly Ala Pro Pro Arg
128          530             535             540
129      gat acc tcg cag agt gac aaa gac ctc gat gat gcc ttg gat aaa ctc    1680
130      Asp Thr Ser Gln Ser Asp Lys Asp Leu Asp Asp Ala Leu Asp Lys Leu
131      545             550             555             560
132      tct gac agt cta gga caa agg cag cct gac cca gat gag aac aaa cca    1728
133      Ser Asp Ser Leu Gly Gln Arg Gln Pro Asp Pro Asp Glu Asn Lys Pro
134              565             570             575
135      atg gga gat aaa gta aag gaa aaa gct aaa gct gaa cat aga gac aag    1776
136      Met Gly Asp Lys Val Lys Glu Lys Ala Lys Ala Glu His Arg Asp Lys
137              580             585             590
138      ctt gga gaa aga gat gac act atc cca cct gaa tac aga cat ctc ctg    1824
139      Leu Gly Glu Arg Asp Asp Thr Ile Pro Pro Glu Tyr Arg His Leu Leu
140              595             600             605
141      gat gat aat gga cag gac aaa cca gtg aag cca cct aca aag aaa tca    1872
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144          gag gat tca aag aaa cct gca gat gac caa gac ccc att gat gct ctc    1920
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147          tca gga gat ctg gac agc tgt ccc tcc act aca gaa acc tca cag aac    1968
148          Ser Gly Asp Leu Asp Ser Cys Pro Ser Thr Thr Glu Thr Ser Gln Asn
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150          aca gca aag gat aag tgc aag aag gct gct tcc agc tcc aaa gca cct    2016
151          Thr Ala Lys Asp Lys Cys Lys Lys Ala Ala Ser Ser Ser Lys Ala Pro
152                    660                665                670
153          aag aat gga ggt aaa gcg aag gat tca gca aag aca aca gag gaa act    2064
154          Lys Asn Gly Gly Lys Ala Lys Asp Ser Ala Lys Thr Thr Glu Glu Thr
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162  <212> TYPE: PRT
163  <213> ORGANISM: Homo sapiens
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169          Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu
170                    35                40                45
171          Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala
172               50                55                60
173          His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu
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178                    100                105                110
179          Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser
180               115                120                125
181          Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp
182               130                135                140
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184          145                150                155                160
185          Thr Thr Tyr Thr Gly Pro Glu Val Ser Asp Pro Met Ser Ser Thr Tyr
186                    165                170                175
187          Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg
188                    180                185                190
189          Glu Leu Leu Ala Lys Lys Glu Gly Ile Thr Gly Pro Pro Ala Asp Ser
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192               210                215                220
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196					245				250				255
197	Ala	Ala	Pro	Pro	Gln	Glu	Lys	Lys	Arg	Lys	Val	Glu	Lys	Asp	Thr	Met
198				260				265				270
199	Ser	Asp	Gln	Ala	Leu	Glu	Ala	Leu	Ser	Ala	Ser	Leu	Gly	Thr	Arg	Gln
200			275				280				285
201	Ala	Glu	Pro	Glu	Leu	Asp	Leu	Arg	Ser	Ile	Lys	Glu	Val	Asp	Glu	Ala
202		290				295				300
203	Lys	Ala	Lys	Glu	Glu	Lys	Leu	Glu	Lys	Cys	Gly	Glu	Asp	Asp	Glu	Thr
204	305				310				315				320
205	Ile	Pro	Ser	Glu	Tyr	Arg	Leu	Lys	Pro	Ala	Thr	Asp	Lys	Asp	Gly	Lys
206				325				330				335
207	Pro	Leu	Leu	Pro	Glu	Pro	Glu	Glu	Lys	Pro	Lys	Pro	Arg	Ser	Glu	Ser
208				340				345				350
209	Glu	Leu	Ile	Asp	Glu	Leu	Ser	Glu	Asp	Phe	Asp	Arg	Ser	Glu	Cys	Lys
210			355				360				365
211	Glu	Lys	Pro	Ser	Lys	Pro	Thr	Glu	Lys	Thr	Glu	Glu	Ser	Lys	Ala	Ala
212		370				375				380
213	Ala	Pro	Ala	Pro	Val	Ser	Glu	Ala	Val	Ser	Arg	Thr	Ser	Met	Cys	Ser
214	385				390				395				400
215	Ile	Gln	Ser	Ala	Pro	Pro	Glu	Pro	Ala	Thr	Leu	Lys	Gly	Thr	Val	Pro
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219	Asp	Pro	Glu	Asp	Gly	Lys	Pro	Val	Met	Asp	Lys	Val	Lys	Glu	Lys	Ala
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229	Ser	Leu	Lys	Phe	Glu	Asp	Ala	Lys	Leu	Ala	Ala	Ala	Ile	Ser	Glu	Val
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231	Val	Ser	Gln	Thr	Pro	Ala	Ser	Thr	Thr	Gln	Ala	Gly	Ala	Pro	Pro	Arg
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234	545				550				555				560
235	Ser	Asp	Ser	Leu	Gly	Gln	Arg	Gln	Pro	Asp	Pro	Asp	Glu	Asn	Lys	Pro
236				565				570				575
237	Met	Gly	Asp	Lys	Val	Lys	Glu	Lys	Ala	Lys	Ala	Glu	His	Arg	Asp	Lys
238			580				585				590
239	Leu	Gly	Glu	Arg	Asp	Asp	Thr	Ile	Pro	Pro	Glu	Tyr	Arg	His	Leu	Leu
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VERIFICATION SUMMARY   DATE: 04/12/2006
PATENT APPLICATION: **US/10/788,489**   TIME: 12:28:50

Input Set : **N:\Crf3\RULE60\10788489.raw**
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L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1